SEQUENCE LISTING

<110> ROJER, EVA

<120> REARRANGED SQUAMOUS CELL CARCINOMA ANTIGEN GENES II

<130> 7274

<140> 10/661,742
<141> 2003-09-12

<150> PCT/SE02/00512
<151> 2002-03-15

<150> SE 0100938
<151> 2001-03-15

<160> 19

<170> PatentIn Ver. 3.3

<210> 1
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
     construct

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Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
              20   25   30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
          35   40   45

Thr Ala Gln Gln Ile Lys Lys Val Leu His Phe Asp Gln Val Thr Glu
     50   55   60

Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
 65   70   75   80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
                 85   90   95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
             100   105   110

Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
         115   120   125

Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
     130   135   140

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Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145             150             155             160

Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
            165             170             175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
            180             185             190

Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
        195             200             205

Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu
    210             215             220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225             230             235             240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
            245             250             255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
            260             265             270

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
        275             280             285

Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
    290             295             300

Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
305             310             315             320

His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
            325             330             335

Thr Glu Glu Gly Val Glu Ala Ala Ala Thr Ala Val Val Val Val
            340             345             350

Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
        355             360             365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
    370             375             380

Gly Arg Phe Ser Ser Pro
385             390
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gtcctcttag gagccaaaga caacactgca caacagatta agaaggttct tcactttgat 180
caagtcacag agaacaccac aggaaaagct gcaacatatc atgttgatag gtcaggaaat 240
gttcatcacc agtttcaaaa gcttctgact gaattcaaca aattccactg atgcatatga 300
gctgaagatc gccaacaagc tcttcggaga aaaaacgtat ctatttttac aggaatattt 360
agatgccatc aagaaatttt accagaccag tgtggaatct gttgattttg caaatgctcc 420
agaagaaagt cgaaagaaga ttaactcctg ggtggaaagt caaacgaatg aaaaaattaa 480
aaacctaatt cctgaaggta atattggcag caataccaca ttggttcttg tgaacgcaat 540
ctatttcaaa gggcagtggg agaagaaatt taataaagaa gatactaaag aggaaaaatt 600
ttggccaaac aagaatacat acaagtccat acagatgatg aggcaataca catcttttca 660
ttttgcctcg ctggaggatg tacaggccaa ggtcctggaa ataccataca aaggcaaaga 720
tctaagcatg attgtgttgc tgccaaatga aatcgatggt ctccagaagc ttgaagagaa 780
actcactgct gagaaattga tggaatggac aagtttgcag aatatgagag agacatgtgt 840
cgatttacac ttacctcggt tcaaaatgga agagagctat gacctcaagg acacgttgag 900
aaccatggga atggtgaata tcttcaatgg ggatgcagac ctctcaggca tgacctggag 960
ccacggtctc tcagtatcta aagtcctaca caaggccttt gtggaggtca ctgaggaggg 1020
agtggaagct gcagctgcca ccgctgtagt agtagtcgaa ttatcatctc cttcaactaa 1080
tgaagagttc tgttgtaatc accctttcct attcttcata aggcaaaata agaccaacag 1140
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<210> 3
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

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<210> 4
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 4
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<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer
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<400> 5
tggaatggac aagtttgcag                                          20


<210> 6
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 6
gtaggactcc agatagcac                                           19


<210> 7
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 7
tggagccacg gtctctcag                                           19


<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 8
attagttgaa ggagatgata attc                                     24


<210> 9
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 9
aatacataca agtcca                                              16
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<210> 10
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 10
ggactttaga tactga                                                        16


<210> 11
<211> 1170
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

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aaatcaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attagggatg 120
gtcctcttag gagccaaaga caacactgca caacagatta agaaggttct tcactttgat 180
caagtcacag agaacaccac aggaaaagct gcaacatatc atgttgatag gtcaggaaat 240
gttcatcacc agtttcaaaa gcttctgact gaattcaaca aatccactga tgcatatgag 300
ctgaagatcg ccaacaagct cttcggagaa aaaacgtatc tattttaca ggaatattta 360
gatgccatca agaaatttta ccagaccagt gtggaatctg ttgattttgc aaatgctcca 420
gaagaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa 480
aacctaattc ctgaaggtaa tattggcagc aataccacat tggttcttgt gaacgcaatc 540
tatttcaaag ggcagtggga gaagaaattt aataaagaag atactaaaga ggaaaaattt 600
tggccaaaca agaatacata caagtccata cagatgatga ggcaatacac atctttcat 660
tttgcctcgc tggaggatgt acaggccaag gtcctggaaa taccatacaa aggcaaagat 720
ctaagcatga ttgtgttgct gccaaatgaa atcgatggtc tccagaagct tgaagagaaa 780
ctcactgctg agaaattgat ggaatggaca agtttgcaga atatgagaga gacatgtgtc 840
gatttacact tacctcggtt caaaatggaa gagagctatg acctcaagga cacgttgaga 900
accatgggaa tggtgaatat cttcaatggg gatgcagacc tctcaggcat gacctggagc 960
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gtggaagctg cagctgccac cgctgtagta gtagtcgaat tatcatctcc ttcaactaat 1080
gaagagttct gttgtaatca ccctttccta ttcttcataa ggcaaaataa gaccaacagc 1140
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<210> 12
<211> 1173
<212> DNA
<213> Homo sapiens

<400> 12
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aaatcaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attagggatg 120
gtcctcttag gagccaaaga caacactgca caacagatta agaaggttct tcactttgat 180
caagtcacag agaacaccac aggaaaagct gcaacatatc atgttgatag gtcaggaaat 240
gttcatcacc agtttcaaaa gcttctgact gaattcaaca aatccactga tgcatatgag 300
ctgaagatcg ccaacaagct cttcggagaa aaaacgtatc tattttaca ggaatattta 360
gatgccatca agaaatttta ccagaccagt gtggaatctg ttgattttgc aaatgctcca 420
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gaagaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa 480
aacctaattc ctgaaggtaa tattggcagc aataccacat tggttcttgt gaacgcaatc 540
tatttcaaag ggcagtggga gaagaaattt aataaagaag atactaaaga ggaaaaattt 600
tggccaaaca agaatacata caagtccata cagatgatga ggcaatacac atcttttcat 660
tttgcctcgc tggaggatgt acaggccaag gtcctggaaa taccatacaa aggcaaagat 720
ctaagcatga ttgtgttgct gccaaatgaa atcgatggtc tccagaagct tgaagagaaa 780
ctcactgctg agaaattgat ggaatggaca agtttgcaga atatgagaga gacacgtgtc 840
gatttacact tacctcggtt caaagtggaa gagagctatg acctcaagga cacgttgaga 900
accatgggaa tggtggatat cttcaatggg gatgcagacc tctcaggcat gaccgggagc 960
cgcggtctcg tgctatctgg agtcctacac aaggcctttg tggaggttac agaggaggga 1020
gcagaagctg cagctgccac cgctgtagta ggattcggat catcacctac ttcaactaat 1080
gaagagttcc attgtaatca ccctttccta ttcttcataa ggcaaaataa gaccaacagc 1140
atcctcttct atggcagatt ctcatccccg tag                          1173
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<210> 13
<211> 1173
<212> DNA
<213> Homo sapiens

<400> 13
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aaatcaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attagggatg 120
gtcctcttag gagccaaaga caacactgca caacaaatta gcaaggttct tcactttgat 180
caagtcacag agaacaccac agaaaaagct gcaacatatc atgttgatag gtcaggaaat 240
gttcatcacc agtttcaaaa gcttctgact gaattcaaca aatccactga tgcatatgag 300
ctgaagatcg ccaacaagct cttcggagaa aagacgtatc aatttttaca ggaatattta 360
gatgccatca agaaatttta ccagaccagt gtggaatcta ctgattttgc aaatgctcca 420
gaagaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa 480
aacctatttc ctgatgggac tattggcaat gatacgacac tggttcttgt gaacgcaatc 540
tatttcaaag ggcagtggga gaataaattt aaaaaagaaa cactaaaga ggaaaaattt 600
tggccaaaca agaatacata caaatctgta cagatgatga ggcaatacaa ttcctttaat 660
tttgccttgc tggaggatgt acaggccaag gtcctggaaa taccatacaa aggcaaagat 720
ctaagcatga ttgtgctgct gccaaatgaa atcgatggtc tgcagaagct tgaagagaaa 780
ctcactgctg agaaattgat ggaatggaca agtttgcaga atatgagaga gacatgtgtc 840
gatttacact tacctcggtt caaaatggaa gagagctatg acctcaagga cacgttgaga 900
accatgggaa tggtgaatat cttcaatggg gatgcagacc tctcaggcat gacctggagc 960
cacggtctct cagtatctaa agtcctacac aaggcctttg tggaggtcac tgaggaggga 1020
gtggaagctg cagctgccac cgctgtagta gtagtcgaat tatcatctcc ttcaactaat 1080
gaagagttct gttgtaatca ccctttccta ttcttcataa ggcaaaataa gaccaacagc 1140
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<210> 14
<211> 390
<212> PRT
<213> Homo sapiens

<400> 14
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 1               5                  10                  15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
             20                  25                  30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
         35                  40                  45
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Thr Ala Gln Gln Ile Lys Lys Val Leu His Phe Asp Gln Val Thr Glu
    50   55   60

Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65   70   75   80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
          85   90   95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
          100   105   110

Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
        115   120   125

Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
        130   135   140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145   150   155   160

Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
        165   170   175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
        180   185   190

Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
        195   200   205

Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu
    210   215   220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225   230   235   240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
        245   250   255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
        260   265   270

Gln Asn Met Arg Glu Thr Arg Val Asp Leu His Leu Pro Arg Phe Lys
        275   280   285

Val Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
    290   295   300

Val Asp Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Gly Ser
305   310   315   320

Arg Gly Leu Val Leu Ser Gly Val Leu His Lys Ala Phe Val Glu Val
        325   330   335

Thr Glu Glu Gly Ala Glu Ala Ala Ala Thr Ala Val Val Gly Phe
        340   345   350

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Gly Ser Ser Pro Ala Ser Thr Asn Glu Glu Phe His Cys Asn His Pro
        355             360             365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
    370             375             380

Gly Arg Phe Ser Ser Pro
385             390


<210> 15
<211> 390
<212> PRT
<213> Homo sapiens

<400> 15
Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
  1           5               10              15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
            20              25              30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
        35              40              45

Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
    50              55              60

Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
 65             70              75              80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
            85              90              95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
            100             105             110

Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
        115             120             125

Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
    130             135             140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145             150             155             160

Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
            165             170             175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
            180             185             190

Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
        195             200             205

Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu
    210             215             220
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```
Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225             230             235             240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
                245             250             255

Leu·Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
            260             265             270

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
            275             280             285

Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
            290             295             300

Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
305             310             315             320

His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
                325             330             335

Thr Glu Glu Gly Val Glu Ala Ala Ala Thr Ala Val Val Val Val
            340             345             350

Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
            355             360             365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
            370             375             380

Gly Arg Phe Ser Ser Pro
385             390
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<210> 16
<211> 1173
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

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aaatcaaaag agaacaacat cttctattcc cctatcagca tcacatcagc attagggatg  120
gtcctcttag gagccaaaga caacactgca caacagatta agaaggttct tcactttgat  180
caagtcacag agaacaccac aggaaaagct gcaacatatc atgttgatag gtcaggaaat  240
gttcatcacc agtttcaaaa gcttctgact gaattcaaca aatccactga tgcatatgag  300
ctgaagatcg ccaacaagct cttcggagaa aaaacgtatc tatttttaca ggaatattta  360
gatgccatca agaaatttta ccagaccagt gtggaatctg ttgattttgc aaatgctcca  420
gaagaaagtc gaaagaagat taactcctgg gtggaaagtc aaacgaatga aaaaattaaa  480
aacctaattc ctgaaggtaa tattggcagc aataccacat ggttcttgt gaacgcaatc  540
tatttcaaag ggcagtggga agaaatttt aataagaag atactaaaga ggaaaaattt  600
tggccaaaca agaatacata caartcyrta cagatgatga ggcaatacam wtcytttmat  660
tttgcctygc tggaggatgt acaggccaag gtcctggaaa taccatacaa aggcaaagat  720
ctaagcatga ttgtgytgct gccaaatgaa atcgatggtc tscagaagct tgaagagaaa  780
ctcactgctg agaaattgat ggaatggaca agtttgcaga atatgagaga gacaygtgtc  840
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gatttacact tacctcggtt caaartggaa gagagctatg acctcaagga cacgttgaga 900
accatgggaa tggtgratat cttcaatggg gatgcagacc tctcaggcat gacckggagc 960
crcggtctck yrstatctrr agtcctacac aaggcctttg tggaggtyac wgaggaggga 1020
gyrgaagctg cagctgccac cgctgtagta gtagtcgaat tatcatctcc ttcaactaat 1080
gaagagttct gttgtaatca ccctttccta ttcttcataa ggcaaaataa gaccaacagc 1140
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<210> 17
<211> 390
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

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<222> (210)
<223> Ile or Val

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<223> Thr or Asn

<220>
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<223> His or Asn

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<223> Ser or Leu

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<223> Arg or Cys

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<223> Val or Met

<220>
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<223> Asp or Asn

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<222> (319)
<223> Gly or Trp

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<220>
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<220>
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<223> Gly or Lys

<220>
<221> MOD_RES
<222> (341)
<223> Ala or Val

<400> 17
Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
 1           5                   10                  15

Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
            20                  25                  30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
            35                  40                  45

Thr Ala Gln Gln Ile Lys Lys Val Leu His Phe Asp Gln Val Thr Glu
        50                  55                  60

Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65                  70                  75                  80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
                85                  90                  95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
            100                 105                 110

Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
            115                 120                 125

Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
        130                 135                 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145                 150                 155                 160

Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
            165                 170                 175
```

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
          180   185   190

Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
          195   200   205

Ser Xaa Gln Met Met Arg Gln Tyr Xaa Ser Phe Xaa Phe Ala Xaa Leu
          210   215   220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225   230   235   240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
              245   250   255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
          260   265   270

Gln Asn Met Arg Glu Thr Xaa Val Asp Leu His Leu Pro Arg Phe Lys
          275   280   285

Xaa Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
    290   295   300

Val Xaa Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Xaa Ser
305   310   315   320

Xaa Gly Leu Xaa Xaa Ser Xaa Val Leu His Lys Ala Phe Val Glu Val
          325   330   335

Thr Glu Glu Gly Xaa Glu Ala Ala Ala Ala Thr Ala Val Val Val Val
          340   345   350

Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
          355   360   365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
    370   375   380

Gly Arg Phe Ser Ser Pro
385   390

<210> 18
<211> 1173
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

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<220>
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            20                  25                  30

Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
        35                  40                  45

Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
    50                  55                  60

Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
 65                  70                  75                  80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
                85                  90                  95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
            100                 105                 110
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Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
    115   120   125

Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
    130   135   140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145   150   155   160

Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
          165   170   175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
        180   185   190

Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
      195   200   205

Ser Xaa Gln Met Met Arg Gln Tyr Xaa Ser Phe Xaa Phe Ala Xaa Leu
    210   215   220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225   230   235   240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
        245   250   255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
      260   265   270

Gln Asn Met Arg Glu Thr Xaa Val Asp Leu His Leu Pro Arg Phe Lys
      275   280   285

Xaa Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
    290   295   300

Val Xaa Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Xaa Ser
305   310   315   320

Xaa Gly Leu Xaa Xaa Ser Xaa Val Leu His Lys Ala Phe Val Glu Val
        325   330   335

Thr Glu Glu Gly Xaa Glu Ala Ala Ala Ala Thr Ala Val Val Gly Phe
        340   345   350

Gly Ser Ser Pro Ala Ser Thr Asn Glu Glu Phe His Cys Asn His Pro
      355   360   365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
      370   375   380

Gly Arg Phe Ser Ser Pro
385   390